L. Specter

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        RAW SEQUENCE LISTING              DATE: 09/22/2000
        PATENT APPLICATION:  US/09/236,468A    TIME: 12:39:27

        Input Set : A:\Pf201dl.txt
        Output Set: N:\CRF3\09222000\I236468A.raw

 3 <110> APPLICANT: Soppet et al.
 5 <120> TITLE OF INVENTION: G-Protein Parathyroid Hormone Receptor HLTDG74
 7 <130> FILE REFERENCE: PF201D1
 9 <140> CURRENT APPLICATION NUMBER: 09/236,468A
10 <141> CURRENT FILING DATE: 1999-01-25
12 <150> PRIOR APPLICATION NUMBER: 08/468,011
13 <151> PRIOR FILING DATE: 1995-06-06
15 <160> NUMBER OF SEQ ID NOS: 28
17 <170> SOFTWARE: PatentIn Ver. 2.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 2003
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
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25 <221> NAME/KEY: CDS
26 <222> LOCATION: (90)..(1715)
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31 ccctgcttct tcctacagcc gttccgggc atg gcc tgg ctg ggg gcg tcg ctc  113
32                                 Met Ala Trp Leu Gly Ala Ser Leu
33                                  1               5
35 cac gtc tgg ggt tgg cta atg ctc ggc agc tgc ctc ctg gcc aga gcc  161
36 His Val Trp Gly Trp Leu Met Leu Gly Ser Cys Leu Leu Ala Arg Ala
37      10              15                  20
39 cag ctg gat tct gat ggc acc atc act ata gag gag cag att gtc ctt  209
40 Gln Leu Asp Ser Asp Gly Thr Ile Thr Ile Glu Glu Gln Ile Val Leu
41  25              30              35                  40
43 gtg ctg aaa gcg aaa gta caa tgt gaa ctc aac atc aca gct caa ctc  257
44 Val Leu Lys Ala Lys Val Gln Cys Glu Leu Asn Ile Thr Ala Gln Leu
45                  45              50                  55
47 cag gag gga gaa ggt aat tgt ttc cct gaa tgg gat gga ctc att tgt  305
48 Gln Glu Gly Glu Gly Asn Cys Phe Pro Glu Trp Asp Gly Leu Ile Cys
49              60                  65                  70
51 tgg ccc aga gga aca gtg ggg aaa ata tcg gct gtt cca tgc cct cct  353
52 Trp Pro Arg Gly Thr Val Gly Lys Ile Ser Ala Val Pro Cys Pro Pro
53          75                  80                  85
55 tat att tat gac ttc aac cat aaa gga gtt gct ttc cga cac tgt aac  401
56 Tyr Ile Tyr Asp Phe Asn His Lys Gly Val Ala Phe Arg His Cys Asn
57      90                  95                  100
59 ccc aat gga aca tgg gat ttt atg cac agc tta aat aaa aca tgg gcc  449
60 Pro Asn Gly Thr Trp Asp Phe Met His Ser Leu Asn Lys Thr Trp Ala
61 105                 110                 115                 120
63 aat tat tca gac tgc ctt cgc ttt ctg cag cca gat atc agc ata gga  497
64 Asn Tyr Ser Asp Cys Leu Arg Phe Leu Gln Pro Asp Ile Ser Ile Gly
65                  125                 130                 135
67 aag caa gaa ttc tgt gaa cgc ctc tat gta atg tat acc gtt ggc tac  545
68 Lys Gln Glu Phe Cys Glu Arg Leu Tyr Val Met Tyr Thr Val Gly Tyr
```

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69          140             145                 150
71 tcc atc tct ttt ggt tcc ttg gct gtg gct att ctc atc att ggt tac   593
72 Ser Ile Ser Phe Gly Ser Leu Ala Val Ala Ile Leu Ile Ile Gly Tyr
73        155                 160                 165
75 ttc aga cga ttg cat tgc act agg aac tat atc cac atg cac tta ttt   641
76 Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met His Leu Phe
77    170                 175                 180
79 gtg tct ttc atg ctg aga gct aca agc atc ttt gtc aaa gac aga gta   689
80 Val Ser Phe Met Leu Arg Ala Thr Ser Ile Phe Val Lys Asp Arg Val
81 185                 190                 195                 200
83 gtc cat gct cac ata gga gta aag gag ctg gag tcc cta ata atg cag   737
84 Val His Ala His Ile Gly Val Lys Glu Leu Glu Ser Leu Ile Met Gln
85            205                 210                 215
87 gat gac cca caa aat tcc att gag gca act tct gtg gac aaa tca caa   785
88 Asp Asp Pro Gln Asn Ser Ile Glu Ala Thr Ser Val Asp Lys Ser Gln
89        220                 225                 230
91 tat atc ggg tgc aag att gct gtt gtg atg ttt att tac ttc ctg gct   833
92 Tyr Ile Gly Cys Lys Ile Ala Val Val Met Phe Ile Tyr Phe Leu Ala
93        235                 240                 245
95 aca aat tat tat tgg atc ctg gtg gaa ggt ctc tac ctg cat aat ctc   881
96 Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu Tyr Leu His Asn Leu
97    250                 255                 260
99 atc ttt gtg gct ttc ttt tcg gac acc aaa tac ctg tgg ggc ttc atc   929
100 Ile Phe Val Ala Phe Phe Ser Asp Thr Lys Tyr Leu Trp Gly Phe Ile
101 265                 270                 275                 280
103 ttg ata ggc tgg ggg ttt cca gca gca ttt gtt gca gca tgg gct gtg   977
104 Leu Ile Gly Trp Gly Phe Pro Ala Ala Phe Val Ala Ala Trp Ala Val
105            285                 290                 295
107 gca cga gca act ctg gct gat gcg agg tgc tgg gaa ctt agt gct gga  1025
108 Ala Arg Ala Thr Leu Ala Asp Ala Arg Cys Trp Glu Leu Ser Ala Gly
109        300                 305                 310
111 gac atc aag tgg att tat caa gca ccg atc tta gca gct att ggg ctg  1073
112 Asp Ile Lys Trp Ile Tyr Gln Ala Pro Ile Leu Ala Ala Ile Gly Leu
113    315                 320                 325
115 aat ttt att ctg ttt ctg aat acg gtt aga gtt cta gct acc aaa atc  1121
116 Asn Phe Ile Leu Phe Leu Asn Thr Val Arg Val Leu Ala Thr Lys Ile
117    330                 335                 340
119 tgg gag acc aat gca gtt ggg cat gac aca agg aag caa tac agg aaa  1169
120 Trp Glu Thr Asn Ala Val Gly His Asp Thr Arg Lys Gln Tyr Arg Lys
121 345                 350                 355                 360
123 ctg gcc aaa tcg aca ctg gtc ctg gtc cta gtc ttt gga gtg cat tac  1217
124 Leu Ala Lys Ser Thr Leu Val Leu Val Leu Val Phe Gly Val His Tyr
125        365                 370                 375
127 atc gtg ttc gtg tgc ctg cct cac tcc ttc act ggg ctc ggg tgg gag  1265
128 Ile Val Phe Val Cys Leu Pro His Ser Phe Thr Gly Leu Gly Trp Glu
129        380                 385                 390
131 atc cgc atg cac tgt gag ctc ttc ttc aac tcc ttt cag ggt ttc ttt  1313
132 Ile Arg Met His Cys Glu Leu Phe Phe Asn Ser Phe Gln Gly Phe Phe
133        395                 400                 405
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135 gtg tct atc atc tac tgc tac tgc aat gga gag gtt cag gca gag gtg  1361
136 Val Ser Ile Ile Tyr Cys Tyr Cys Asn Gly Glu Val Gln Ala Glu Val
137     410             415                 420
139 aag aag atg tgg agt cgg tgg aat ctc tcc gtg gac tgg aaa agg aca  1409
140 Lys Lys Met Trp Ser Arg Trp Asn Leu Ser Val Asp Trp Lys Arg Thr
141 425             430                 435                 440
143 ccg cca tgt ggc agc cgc aga tgc ggc tca gtg ctc acc acc gtg acg  1457
144 Pro Pro Cys Gly Ser Arg Arg Cys Gly Ser Val Leu Thr Thr Val Thr
145             445                 450                 455
147 cac agc acc agc agc cag tca cag gtg gcg gca gca cac gca tgg tgc  1505
148 His Ser Thr Ser Ser Gln Ser Gln Val Ala Ala Ala His Ala Trp Cys
149             460                 465                 470
151 tta tct ctg gca aag ctg cca aga tcg cca gca gac agc ctg aca gcc  1553
152 Leu Ser Leu Ala Lys Leu Pro Arg Ser Pro Ala Asp Ser Leu Thr Ala
153             475                 480                 485
155 aca tca ctt tac ctg gct atg tct gga gta act cag agc agg act gcc  1601
156 Thr Ser Leu Tyr Leu Ala Met Ser Gly Val Thr Gln Ser Arg Thr Ala
157     490                 495                 500
159 tca cac act ctc tcc acg agg agc aac aag gaa gat agt ggg agg cag  1649
160 Ser His Thr Leu Ser Thr Arg Ser Asn Lys Glu Asp Ser Gly Arg Gln
161 505             ·510                515                 520
163 aga gat gat att cta atg gag aag cct tcc agg cct atg gaa tct aac  1697
164 Arg Asp Asp Ile Leu Met Glu Lys Pro Ser Arg Pro Met Glu Ser Asn
165             525                 530                 535
167 cca gac act gaa gga tgácaaggag aaactgagga tgttctctga atggacatgt  1752
168 Pro Asp Thr Glu Gly
169             540
171 gtggctgact ttcatgggct ggtccaatgg ctggttgtgt gagagggctt ggctgatact 1812
173 cctatgcttg agcacaaagg ctgaaaattc agttaaggtg ttacttaata atagtttta  1872
175 ggctccatga attggctcct gtaaatacta acgacatgaa aatgcaagtg tcaatggagt 1932
177 agtttattac cttctattgg catcaagttt tcctctaaat taatgtatgt tatttgctct 1992
179 gtgattgttc a                                                      2003
182 <210> SEQ ID NO: 2
183 <211> LENGTH: 541
184 <212> TYPE: PRT
185 <213> ORGANISM: Homo sapiens
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191 Gly Ser Cys Leu Leu Ala Arg Ala Gln Leu Asp Ser Asp Gly Thr Ile
192             20                  25                  30
194 Thr Ile Glu Glu Gln Ile Val Leu Val Leu Lys Ala Lys Val Gln Cys
195     35                  40                  45
197 Glu Leu Asn Ile Thr Ala Gln Leu Gln Glu Gly Glu Gly Asn Cys Phe
198     50                  55                  60
200 Pro Glu Trp Asp Gly Leu Ile Cys Trp Pro Arg Gly Thr Val Gly Lys
201 65              70                  75                  80
203 Ile Ser Ala Val Pro Cys Pro Pro Tyr Ile Tyr Asp Phe Asn His Lys
204             85                  90                  95
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206 Gly Val Ala Phe Arg His Cys Asn Pro Asn Gly Thr Trp Asp Phe Met
207           100                   105                   110
209 His Ser Leu Asn Lys Thr Trp Ala Asn Tyr Ser Asp Cys Leu Arg Phe
210           115                   120                   125
212 Leu Gln Pro Asp Ile Ser Ile Gly Lys Gln Glu Phe Cys Glu Arg Leu
213       130                   135                   140
215 Tyr Val Met Tyr Thr Val Gly Tyr Ser Ile Ser Phe Gly Ser Leu Ala
216 145                   150                   155                   160
218 Val Ala Ile Leu Ile Ile Gly Tyr Phe Arg Arg Leu His Cys Thr Arg
219               165                   170                   175
221 Asn Tyr Ile His Met His Leu Phe Val Ser Phe Met Leu Arg Ala Thr
222           180                   185                   190
224 Ser Ile Phe Val Lys Asp Arg Val Val His Ala His Ile Gly Val Lys
225           195                   200                   205
227 Glu Leu Glu Ser Leu Ile Met Gln Asp Asp Pro Gln Asn Ser Ile Glu
228       210                   215                   220
230 Ala Thr Ser Val Asp Lys Ser Gln Tyr Ile Gly Cys Lys Ile Ala Val
231 225                   230                   235                   240
233 Val Met Phe Ile Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val
234               245                   250                   255
236 Glu Gly Leu Tyr Leu His Asn Leu Ile Phe Val Ala Phe Phe Ser Asp
237           260                   265                   270
239 Thr Lys Tyr Leu Trp Gly Phe Ile Leu Ile Gly Trp Gly Phe Pro Ala
240           275                   280                   285
242 Ala Phe Val Ala Ala Trp Ala Val Ala Arg Ala Thr Leu Ala Asp Ala
243       290                   295                   300
245 Arg Cys Trp Glu Leu Ser Ala Gly Asp Ile Lys Trp Ile Tyr Gln Ala
246 305                   310                   315                   320
248 Pro Ile Leu Ala Ala Ile Gly Leu Asn Phe Ile Leu Phe Leu Asn Thr
249               325                   330                   335
251 Val Arg Val Leu Ala Thr Lys Ile Trp Glu Thr Asn Ala Val Gly His
252           340                   345                   350
254 Asp Thr Arg Lys Gln Tyr Arg Lys Leu Ala Lys Ser Thr Leu Val Leu
255           355                   360                   365
257 Val Leu Val Phe Gly Val His Tyr Ile Val Phe Val Cys Leu Pro His
258       370                   375                   380
260 Ser Phe Thr Gly Leu Gly Trp Glu Ile Arg Met His Cys Glu Leu Phe
261 385                   390                   395                   400
263 Phe Asn Ser Phe Gln Gly Phe Phe Val Ser Ile Ile Tyr Cys Tyr Cys
264               405                   410                   415
266 Asn Gly Glu Val Gln Ala Glu Val Lys Lys Met Trp Ser Arg Trp Asn
267           420                   425                   430
269 Leu Ser Val Asp Trp Lys Arg Thr Pro Pro Cys Gly Ser Arg Arg Cys
270           435                   440                   445
272 Gly Ser Val Leu Thr Thr Val Thr His Ser Thr Ser Ser Gln Ser Gln
273       450                   455                   460
275 Val Ala Ala Ala His Ala Trp Cys Leu Ser Leu Ala Lys Leu Pro Arg
276 465                   470                   475                   480
278 Ser Pro Ala Asp Ser Leu Thr Ala Thr Ser Leu Tyr Leu Ala Met Ser
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279            485            490            495
281 Gly Val Thr Gln Ser Arg Thr Ala Ser His Thr Leu Ser Thr Arg Ser
282            500            505            510
284 Asn Lys Glu Asp Ser Gly Arg Gln Arg Asp Asp Ile Leu Met Glu Lys
285        515            520            525
287 Pro Ser Arg Pro Met Glu Ser Asn Pro Asp Thr Glu Gly
288     530            535            540
292 <210> SEQ ID NO: 3
293 <211> LENGTH: 23
294 <212> TYPE: DNA
295 <213> ORGANISM: Artificial Sequence
297 <220> FEATURE:
298 <221> NAME/KEY: Primer_Bind
299 <223> OTHER INFORMATION: This 5' primer sequence contains a SmaI restriction
300        enzyme site followed by nucleotides corresponding to PTH receptor
301        coding sequence.
303 <400> SEQUENCE: 3
304 cagccgtccc gggcttggcc tgg                                        23
307 <210> SEQ ID NO: 4
308 <211> LENGTH: 27
309 <212> TYPE: DNA
310 <213> ORGANISM: Artificial Sequence
312 <220> FEATURE:
313 <221> NAME/KEY: Primer_Bind
314 <223> OTHER INFORMATION: This 3' primer sequence contains a SalI restriction
315        enzyme site and a sequence complementary to the human PTH
316        receptor.
318 <400> SEQUENCE: 4
319 cctcagtgtc gacttgtcat ccttcag                                    27
322 <210> SEQ ID NO: 5
323 <211> LENGTH: 27
324 <212> TYPE: DNA
325 <213> ORGANISM: Artificial Sequence
327 <220> FEATURE:
328 <221> NAME/KEY: Primer_Bind
329 <223> OTHER INFORMATION: This 5' primer contains a HindIII restriction enzyme site
330        and a nucleotide sequence corresponding to the 5' UTR of the cDNA
331        encoding human PTH receptor.
333 <400> SEQUENCE: 5
334 gttggcatat tggaagcttt ttgcggg                                    27
337 <210> SEQ ID NO: 6
338 <211> LENGTH: 28
339 <212> TYPE: DNA
340 <213> ORGANISM: Artificial Sequence
342 <220> FEATURE:
343 <221> NAME/KEY: Primer_Bind
344 <223> OTHER INFORMATION: This 3' primer sequence contains an XbaI restriction
345        enzyme site, a translation stop codon, and nucleotides
346        complementary to the human PTH receptor coding sequence.
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VERIFICATION SUMMARY   DATE: 09/22/2000
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